

# SEQUENCE LISTING

<110> Kruse, Daniela  
Hertmann, Thomas  
Thierbach, Georg  
Rieping, Mechthild

<120> A Process for Preparing L-Threonione

<130> 7601/88025

<140> 10/567749

<141> 2006-02-10

<160> 10

<170> PatentIn version 3.4

<210> 1

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<222> (1)..(990)

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Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Glu Leu Leu Ser Gln	
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gga gcc aca cag cgt gtg ttg gac gcg act cag ctt tac ctt ggt gag	192
Gly Ala Thr Gln Arg Val Leu Asp Ala Thr Gln Leu Tyr Leu Gly Glu	
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Ile Gly Tyr Ser Pro Leu Leu Thr Ala Glu Glu Glu Val Tyr Phe Ala	
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Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu	
85 90 95	
agt aac ttg cgt ctg gtg gta aaa att gcc cgc cgt tat ggc aat cgt	336
Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg	
100 105 110	
ggt ctg gcg ttg ctg gac ctt atc gaa gag ggc aac ctg ggg ctg atc	384
Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile	
115 120 125	

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cca agt gcg gaa gag atc gca gag caa ctg gat aag cca gtt gat gac Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp 195 200 205	624
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325

330

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Gln	Thr	Arg	Thr	Ile	Arg	Leu	Pro	Ile	His	Ile	Val	Lys	Glu	Leu	Asn
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Pro	Ser	Ala	Glu	Glu	Ile	Ala	Glu	Gln	Leu	Asp	Lys	Pro	Val	Asp	Asp
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Pro	Leu	Gly	Gly	Asp	Ser	Glu	Lys	Ala	Leu	Leu	Asp	Ile	Leu	Ala	Asp
225					230					235					240
Glu	Lys	Glu	Asn	Gly	Pro	Glu	Asp	Thr	Thr	Gln	Asp	Asp	Asp	Met	Lys
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Val	Leu	Ala	Arg	Arg	Phe	Gly	Leu	Leu	Gly	Tyr	Glu	Ala	Ala	Thr	Leu
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Glu	Asp	Val	Gly	Arg	Glu	Ile	Gly	Leu	Thr	Arg	Glu	Arg	Val	Arg	Gln
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Ile	Gln	Val	Glu	Gly	Leu	Arg	Arg	Leu	Arg	Glu	Ile	Leu	Gln	Thr	Gln
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 gccgaagagg aactgttata gcagggagcc acacagcgtg tggtggacgc gactcagctt 180  
 taccttggtg agattggtta ttcaccactg ttaacggccg aagaagaagt ttattttgcg 240  
 cgtcgcgcac tgcgtggaga tgtcgcctct cgccgccgga tgatcgagag taacttgcg 300  
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 gaagagggca acctggggct gatccgcgcg gtagagaagt ttgacccgga acgtggtttc 420  
 cgcttctcaa catacgaac ctggtggatt cgccagacga ttgaacgggc gattatgaac 480  
 caaaccgta ctattcgttt gccgattcac atcgtaaagg agctgaacgt ttacctgcga 540  
 accgcacgtg agttgtccca taagctggac catgaaccaa gtgcggaaga gatcgagag 600  
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 gaaaaagaga acggtccgga agataccacg caagatgacg atatgaagca gagcatcgtc 780  
 aatggctgt tcgagctgaa cgccaaacag cgtgaagtgc tggcacgtcg attcggtttg 840  
 ctgggggtacg aagcggcaac actggaagat gtaggtcgtg aaattggcct caccctgaa 900  
 cgtgttcgcc agattcaggt tgaaggcctg cgccgtttgc gcgaaatcct gcaaacgcag 960  
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 Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr  
 20 25 30  
 ccg cta caa aaa atg gaa aaa ctg tcg tcg cgt ctt gat aac gtc att 144  
 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile  
 35 40 45  
 ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc 192  
 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg  
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 ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac 240  
 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His  
 65 70 75 80  
 ggc gtg atc act gct tct gcg ggt aac cac gcg cag ggc gtc gcg ttt 288  
 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe  
 85 90 95  
 tct tct gcg cgg tta ggc gtg aag gcc ctg atc gtt atg cca acc gcc 336  
 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala  
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 acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg 384  
 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val  
 115 120 125  
 ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa 432  
 Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu  
 130 135 140  
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 Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro  
 145 150 155 160  
 atg gtg att gcc ggg caa ggc acg ctg gcg ctg gaa ctg ctc cag cag 528  
 Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln  
 165 170 175

gac gcc cat ctc gac cgc gta ttt gtg cca gtc ggc ggc ggc ggt ctg Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu	576
180 185 190	
gct gct ggc gtg gcg gtg ctg atc aaa caa ctg atg ccg caa atc aaa Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys	624
195 200 205	
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210 215 220	
gat gcg ggt cat ccg gtt gat ctg ccg cgc gta ggg cta ttt gct gaa Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu	720
225 230 235 240	
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245 250 255	
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260 265 270	
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275 280 285	
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290 295 300	
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325 330 335	
cgt gaa gcg ttg ttg gcg gtg acc att ccg gaa gaa aaa ggc agc ttc Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe	1056
340 345 350	
ctc aaa ttc tgc caa ctg ctt ggc ggc cgt tcg gtc acc gag ttc aac Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn	1104
355 360 365	
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370 375 380	
ctg agc cgc ggc ctc gaa gag cgc aaa gaa att ttg cag atg ctc aac Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn	1200
385 390 395 400	
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gaa cgc ctc tac agc ttc gaa ttc ccg gaa tca ccg ggc gcg ctg ctg	1344
Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu	
435 440 445	
cgc ttc ctc aac acg ctg ggt acg tac tgg aac att tct ttg ttc cac	1392
Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His	
450 455 460	
tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa	1440
Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu	
465 470 475 480	
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Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly	
485 490 495	
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Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His	
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Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe	
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Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala	
100 105 110	
Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val	
115 120 125	
Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu	
130 135 140	

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Asp	Ala	His	Leu	Asp	Arg	Val	Phe	Val	Pro	Val	Gly	Gly	Gly	Gly	Leu
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Val	Ile	Ala	Val	Glu	Ala	Glu	Asp	Ser	Ala	Cys	Leu	Lys	Ala	Ala	Leu
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Glu	Tyr	Leu	Asp	Asp	Ile	Ile	Thr	Val	Asp	Ser	Asp	Ala	Ile	Cys	Ala
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Ala	Met	Lys	Asp	Leu	Phe	Glu	Asp	Val	Arg	Ala	Val	Ala	Glu	Pro	Ser
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Gly	Ala	Leu	Ala	Leu	Ala	Gly	Met	Lys	Lys	Tyr	Ile	Ala	Leu	His	Asn
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Asp	Gly	Gly	Tyr	Ser	Val	Val	Asp	Leu	Ser	Asp	Asp	Glu	Met	Ala	Lys
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Leu	His	Val	Arg	Tyr	Met	Val	Gly	Gly	Arg	Pro	Ser	His	Pro	Leu	Gln
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	450					455					460				



Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu  
465 470 475 480

Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly  
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Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu  
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Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr  
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Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile  
35 40 45  
ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc 192  
Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg  
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ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac 240  
Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His  
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Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe  
85 90 95  
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Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala  
100 105 110  
acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg 384  
Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val  
115 120 125  
ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa 432

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Leu	Ser	Gln	Gln	Gln	Gly	Phe	Thr	Trp	Val	Pro	Pro	Phe	Asp	His	Pro	
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Met	Val	Ile	Ala	Gly	Gln	Gly	Thr	Leu	Ala	Leu	Glu	Leu	Leu	Gln	Gln	
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Asp	Ala	His	Leu	Asp	Arg	Val	Phe	Val	Pro	Val	Gly	Gly	Gly	Gly	Leu	
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Ala	Ala	Gly	Val	Ala	Val	Leu	Ile	Lys	Gln	Leu	Met	Pro	Gln	Ile	Lys	
		195					200					205				
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Val	Ile	Ala	Val	Glu	Ala	Glu	Asp	Ser	Ala	Cys	Leu	Lys	Ala	Ala	Leu	
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Asp	Ala	Gly	His	Pro	Val	Asp	Leu	Pro	Arg	Val	Gly	Leu	Phe	Ala	Glu	
225					230					235					240	
ggc	gta	gcg	gta	aaa	cgc	atc	ggg	gac	gaa	acc	ttc	cgt	tta	tgc	cag	768
Gly	Val	Ala	Val	Lys	Arg	Ile	Gly	Asp	Glu	Thr	Phe	Arg	Leu	Cys	Gln	
				245					250					255		
gag	tat	ctc	gac	gac	atc	atc	acc	gtc	gat	agc	gat	gcg	atc	tgt	gcg	816
Glu	Tyr	Leu	Asp	Asp	Ile	Ile	Thr	Val	Asp	Ser	Asp	Ala	Ile	Cys	Ala	
			260					265					270			
gcg	atg	aag	gat	tta	ttc	gaa	gat	gtg	cgc	gcg	gtg	gcg	aaa	ccc	tct	864
Ala	Met	Lys	Asp	Leu	Phe	Glu	Asp	Val	Arg	Ala	Val	Ala	Lys	Pro	Ser	
		275					280					285				
ggc	gcg	ctg	gcg	ctg	gcg	gga	atg	aaa	aaa	tat	atc	gcc	ctg	cac	aac	912
Gly	Ala	Leu	Ala	Leu	Ala	Gly	Met	Lys	Lys	Tyr	Ile	Ala	Leu	His	Asn	
	290					295					300					
att	cgc	ggc	gaa	cgg	ctg	gcg	cat	att	ctt	tcc	ggg	gcc	aac	gtg	aac	960
Ile	Arg	Gly	Glu	Arg	Leu	Ala	His	Ile	Leu	Ser	Gly	Ala	Asn	Val	Asn	
305					310					315					320	
ttc	cac	ggc	ctg	cgc	tac	gtc	tca	gaa	cgc	tgc	gaa	ctg	ggc	gaa	cag	1008
Phe	His	Gly	Leu	Arg	Tyr	Val	Ser	Glu	Arg	Cys	Glu	Leu	Gly	Glu	Gln	
				325					330					335		
cgt	gaa	gcg	ttg	ttg	gcg	gtg	acc	att	ccg	gaa	gaa	aaa	ggc	agc	ttc	1056
Arg	Glu	Ala	Leu	Leu	Ala	Val	Thr	Ile	Pro	Glu	Glu	Lys	Gly	Ser	Phe	
			340					345					350			
ctc	aaa	ttc	tgc	caa	ctg	ctt	ggc	ggg	cgt	tgc	gtc	acc	gag	ttc	aac	1104
Leu	Lys	Phe	Cys	Gln	Leu	Leu	Gly	Gly	Arg	Ser	Val	Thr	Glu	Phe	Asn	
		355					360					365				

tac cgt ttt gcc gat gcc aaa aac gcc tgc atc ttt gtc ggt gtg cgc Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg 370 375 380	1152
ctg agc cgc ggc ctc gaa gag cgc aaa gaa att ttg cag atg ctc aac Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn 385 390 395 400	1200
gac ggc ggc tac agc gtg gtt gat ctc tcc gac gac gaa atg gcg aag Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys 405 410 415	1248
cta cac gtg cgc tat atg gtc ggc gga cgt cca tcg cat ccg ttg cag Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln 420 425 430	1296
gaa cgc ctc tac agc ttc gaa ttc ccg gaa tca ccg ggc gcg ctg ctg Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu 435 440 445	1344
cgc ttc ctc aac acg ctg ggt acg tac tgg aac att tct ttg ttc cac Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His 450 455 460	1392
tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu 465 470 475 480	1440
ctt ggc gac cat gaa ccg gat ttc gaa acc cgg ctg aat gag ctg ggc Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly 485 490 495	1488
tac gat tgc cac gac gaa acc aat aac ccg gcg ttc agg ttc ttt ttg Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu 500 505 510	1536
gcg ggt tag Ala Gly	1545

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 <213> Escherichia coli

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 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile  
 35 40 45  
 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg  
 50 55 60  
 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His  
 65 70 75 80

Gly	Val	Ile	Thr	Ala	Ser	Ala	Gly	Asn	His	Ala	Gln	Gly	Val	Ala	Phe	85	90	95
Ser	Ser	Ala	Arg	Leu	Gly	Val	Lys	Ala	Leu	Ile	Val	Met	Pro	Thr	Ala	100	105	110
Thr	Ala	Asp	Ile	Lys	Val	Asp	Ala	Val	Arg	Gly	Phe	Gly	Gly	Glu	Val	115	120	125
Leu	Leu	His	Gly	Ala	Asn	Phe	Asp	Glu	Ala	Lys	Ala	Lys	Ala	Ile	Glu	130	135	140
Leu	Ser	Gln	Gln	Gln	Gly	Phe	Thr	Trp	Val	Pro	Pro	Phe	Asp	His	Pro	145	150	155
Met	Val	Ile	Ala	Gly	Gln	Gly	Thr	Leu	Ala	Leu	Glu	Leu	Leu	Gln	Gln	165	170	175
Asp	Ala	His	Leu	Asp	Arg	Val	Phe	Val	Pro	Val	Gly	Gly	Gly	Gly	Leu	180	185	190
Ala	Ala	Gly	Val	Ala	Val	Leu	Ile	Lys	Gln	Leu	Met	Pro	Gln	Ile	Lys	195	200	205
Val	Ile	Ala	Val	Glu	Ala	Glu	Asp	Ser	Ala	Cys	Leu	Lys	Ala	Ala	Leu	210	215	220
Asp	Ala	Gly	His	Pro	Val	Asp	Leu	Pro	Arg	Val	Gly	Leu	Phe	Ala	Glu	225	230	235
Gly	Val	Ala	Val	Lys	Arg	Ile	Gly	Asp	Glu	Thr	Phe	Arg	Leu	Cys	Gln	245	250	255
Glu	Tyr	Leu	Asp	Asp	Ile	Ile	Thr	Val	Asp	Ser	Asp	Ala	Ile	Cys	Ala	260	265	270
Ala	Met	Lys	Asp	Leu	Phe	Glu	Asp	Val	Arg	Ala	Val	Ala	Lys	Pro	Ser	275	280	285
Gly	Ala	Leu	Ala	Leu	Ala	Gly	Met	Lys	Lys	Tyr	Ile	Ala	Leu	His	Asn	290	295	300
Ile	Arg	Gly	Glu	Arg	Leu	Ala	His	Ile	Leu	Ser	Gly	Ala	Asn	Val	Asn	305	310	315
Phe	His	Gly	Leu	Arg	Tyr	Val	Ser	Glu	Arg	Cys	Glu	Leu	Gly	Glu	Gln	325	330	335
Arg	Glu	Ala	Leu	Leu	Ala	Val	Thr	Ile	Pro	Glu	Glu	Lys	Gly	Ser	Phe	340	345	350
Leu	Lys	Phe	Cys	Gln	Leu	Leu	Gly	Gly	Arg	Ser	Val	Thr	Glu	Phe	Asn	355	360	365
Tyr	Arg	Phe	Ala	Asp	Ala	Lys	Asn	Ala	Cys	Ile	Phe	Val	Gly	Val	Arg	370	375	380
Leu	Ser	Arg	Gly	Leu	Glu	Glu	Arg	Lys	Glu	Ile	Leu	Gln	Met	Leu	Asn	385	390	395
																		400

Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys  
 405 410 415  
 Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln  
 420 425 430  
 Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu  
 435 440 445  
 Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His  
 450 455 460  
 Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu  
 465 470 475 480  
 Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly  
 485 490 495  
 Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu  
 500 505 510

Ala Gly

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 <213> Escherichia coli

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 gagtctgttc aagctgaccg aaacggatca gcgcatacc attggtctga acctgccttc 180  
 tggcgagatg ggccgcaaag atctgatcaa aatcgaaaat acctttttga gtgaagatca 240  
 agtagatcaa ctggcattgt atgcgccgca agccacgggt aaccgtatcg acaactatga 300  
 agtgggtgggt aaatcgcgcc caagtctgcc ggagcgcata gacaatgtgc tggctctgcc 360  
 gaacagcaac tgtatcagcc atgccgaacc ggtttcatcc agcttttgccg tgcgaaaacg 420  
 cgccaatgat atcgcgctca aatgcaaata ctgtgaaaaa gagttttccc ataatgtggt 480  
 gctggccaat taattgcggt tggtaataaa agtctggctc cctata atg agc cag 535  
 Met Ser Gln  
 1  
 act ttt tac cgc tgt aat aaa gga gaa atc atg agc aaa act atc gcg 583  
 Thr Phe Tyr Arg Cys Asn Lys Gly Glu Ile Met Ser Lys Thr Ile Ala  
 5 10 15  
 acg gaa aat gca ccg gca gct atc ggt cct tac gta cag ggc gtt gat 631

Thr	Glu	Asn	Ala	Pro	Ala	Ala	Ile	Gly	Pro	Tyr	Val	Gln	Gly	Val	Asp	
20					25				30						35	
ctg	ggc	aat	atg	atc	atc	acc	tcc	ggt	cag	atc	ccg	gta	aat	ccg	aaa	679
Leu	Gly	Asn	Met	Ile	Ile	Thr	Ser	Gly	Gln	Ile	Pro	Val	Asn	Pro	Lys	
				40				45					50			
acg	ggc	gaa	gta	ccg	gca	gac	gtc	gct	gca	cag	gca	cgt	cag	tcg	ctg	727
Thr	Gly	Glu	Val	Pro	Ala	Asp	Val	Ala	Ala	Gln	Ala	Arg	Gln	Ser	Leu	
			55				60					65				
gat	aac	gta	aaa	gcg	atc	gtc	gaa	gcc	gct	ggc	ctg	aaa	gtg	ggc	gac	775
Asp	Asn	Val	Lys	Ala	Ile	Val	Glu	Ala	Ala	Gly	Leu	Lys	Val	Gly	Asp	
		70				75					80					
atc	gtt	aaa	act	acc	gtg	ttt	gta	aaa	gat	ctg	aac	gac	ttc	gca	acc	823
Ile	Val	Lys	Thr	Thr	Val	Phe	Val	Lys	Asp	Leu	Asn	Asp	Phe	Ala	Thr	
	85					90				95						
gta	aac	gcc	act	tac	gaa	gcc	ttc	ttc	acc	gaa	cac	aac	gcc	acc	ttc	871
Val	Asn	Ala	Thr	Tyr	Glu	Ala	Phe	Phe	Thr	Glu	His	Asn	Ala	Thr	Phe	
100					105				110					115		
ccg	gca	cgt	tct	tgc	gtt	gaa	gtt	gcc	cgt	ctg	ccg	aaa	gac	gtg	aag	919
Pro	Ala	Arg	Ser	Cys	Val	Glu	Val	Ala	Arg	Leu	Pro	Lys	Asp	Val	Lys	
				120				125					130			
att	gag	atc	gaa	gcg	atc	gct	gtt	cgt	cgc	taa	tcttgatgga	aatccgggct				972
Ile	Glu	Ile	Glu	Ala	Ile	Ala	Val	Arg	Arg							
			135			140										
atcatgcccg	gattaagtct	gatgacaaac	gcaaaatcgc	ctgatgcgct	acgcttatca											1032
ggcctacgtg	attcctgcaa	tttattgaat	ttgttgccg	gataaggcat	ttacgccgca											1092
tccggcatga	acaaaactca	ctttgtctac	aatctgaatc	ggggctatcg	tgcccagttt											1152
attctttatt	gccagccgta	acgacggcta	tagaaccctt	tcaccaactg	ggttaatgtc											1212
atataccctg	ccagaatcgc	aaccagccac	gggaaatagc	ttaacggcag	cgcctgtaat											1272
tgcagataac	tggccagcgg	tgaaaacggc	aatgcgatcc	cgacaatcat	cacgatcacg											1332
gtcatgatca	ttaacggcca	cgatgcacag	ctctgaataa	acggcacacg	gcgggtgcgg											1392
atcatatgca	caatcagcgt	ttgcgacagt	aagcccacca	caaaccatcc	cgactggaac											1452
agcgtttgcg	tttccggcgt	gttggcatgg	aatacccacc	acatcaggca	aaacgtcaaa											1512
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<400> 10  
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			20					25					30		
Gly	Val	Asp	Leu	Gly	Asn	Met	Ile	Ile	Thr	Ser	Gly	Gln	Ile	Pro	Val
		35					40					45			
Asn	Pro	Lys	Thr	Gly	Glu	Val	Pro	Ala	Asp	Val	Ala	Ala	Gln	Ala	Arg
		50				55					60				
Gln	Ser	Leu	Asp	Asn	Val	Lys	Ala	Ile	Val	Glu	Ala	Ala	Gly	Leu	Lys
65					70					75					80
Val	Gly	Asp	Ile	Val	Lys	Thr	Thr	Val	Phe	Val	Lys	Asp	Leu	Asn	Asp
				85					90					95	
Phe	Ala	Thr	Val	Asn	Ala	Thr	Tyr	Glu	Ala	Phe	Phe	Thr	Glu	His	Asn
			100					105					110		
Ala	Thr	Phe	Pro	Ala	Arg	Ser	Cys	Val	Glu	Val	Ala	Arg	Leu	Pro	Lys
		115					120					125			
Asp	Val	Lys	Ile	Glu	Ile	Glu	Ala	Ile	Ala	Val	Arg	Arg			
	130					135					140				